

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL
PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0213 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Val	Lys	Tyr	Phe	Leu	Gly	Gln	Ser	Val	Leu	Arg	Ser	Ser	Trp	Asp
1				5				10						15	
Gln	Val	Phe	Ala	Ala	Phe	Trp	Gln	Arg	Tyr	Pro	Asn	Pro	Tyr	Ser	Lys
			20				25						30		

[illegible]

His	Val	Leu	Thr	Glu	Asp	Ile	Val	His	Arg	Glu	Val	Thr	Pro	Asp	Gln
		35					40					45			
Lys	Leu	Leu	Ser	Arg	Arg	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Met	Pro	Arg
	50					55					60				
Trp	Ala	Glu	Arg	Leu	Phe	Pro	Ala	Asn	Val	Ala	His	Ser	Val	Tyr	Val
65					70					75					80
Leu	Glu	Asp	Ser	Ile	Val	Asp	Pro	Gln	Asn	Gln	Thr	Met	Thr	Thr	Phe
				85					90					95	
Thr	Trp	Asn	Ile	Asn	His	Ala	Arg	Leu	Met	Val	Val	Glu	Glu	Arg	Cys
			100					105					110		
Val	Tyr	Cys	Val	Asn	Ser	Asp	Asn	Ser	Gly	Trp	Thr	Glu	Ile	Arg	Arg
		115					120					125			
Glu	Ala	Trp	Val	Ser	Ser	Ser	Leu	Phe	Gly	Val	Ser	Arg	Ala	Val	Gln
		130				135					140				
Glu	Phe	Gly	Leu	Ala	Arg	Phe	Lys	Ser	Asn	Val	Thr	Lys	Thr	Met	Lys
145					150					155					160
Gly	Phe	Glu	Tyr	Ile	Leu	Ala	Lys	Leu	Gln	Gly	Glu	Ala	Pro	Ser	Lys
				165					170					175	
Thr	Leu	Val	Glu	Thr	Ala	Lys	Glu	Ala	Lys	Glu	Lys	Ala	Lys	Glu	Thr
			180					185					190		
Ala	Leu	Ala	Ala	Thr	Glu	Lys	Ala	Lys	Asp	Leu	Ala	Ser	Lys	Ala	Ala
		195					200					205			
Thr	Lys	Lys	Gln	Gln	Gln	Gln	Gln	Gln	Phe	Val					
	210					215									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGTGGTGA	CTGAGCTACG	AGCCTGGCGG	CGGGTGTGCG	CCGAGCCCCG	GCCCGGCCCG	60
GCCCTCGCGT	GCCTCCCAGG	CTCCGCACCC	CTGATGCTGC	GCGGGTGCTG	AGCCCGCTTC	120
GGCCGGGACG	ATGGTGAAGT	ATTTCTTGGG	CCAGAGCGTG	CTCCGGAGTT	CCTGGGACCA	180
AGTGTTCGCG	GCCTTCTGGC	AGCGGTACCC	GAATCCCTAT	AGCAAACATG	TCTTGGACGA	240
AGACATAGTA	CACCGGGAGG	TGACCCCTGA	CCAGAAACTG	CTGTCCCGCG	GACTCCTGAC	300
CAAGACCAAC	AGGATGCCAC	GCTGGGCCGA	GCGACTATTT	CCTGCCAATG	TTGCTCACTC	360
GGTGTACGTC	CTGGAGGACT	CTATTGTGGA	CCCACAGAAT	CAGACCATGA	CTACCTTCAC	420
CTGGAACATC	AACCACGCC	GGCTGATGGT	GGTGGAGGAA	CGATGTGTTT	ACTGTGTGAA	480
CCTTGACAAC	AGTGGCTGGA	CTGAAATCCG	CCGGGAAGAC	TGGGTCTCCT	CTAGCTTATT	540
TGGTGTCTCC	AGAGCTGTCC	AGGAATTTGG	CTTTGCCCGG	TTCAAAAGCA	ACGTGACCAA	600
GACTATGAAG	GGTTTTGAAT	ATATCTTGGC	TAAGCTGCAA	GGCGAGGCC	CTTCCAAAAC	660
ACTTGTTGAG	ACAGCCAAGG	AAGCCAAGGA	GAAGGCAAAG	GAGACGGCAC	TGGCAGCTAC	720
AGAGAAGGCC	AAGGACCTCG	CCAGCAAGGC	GGCCACCAAG	AAGCAGCAGC	AGCAGCAACA	780
GTTTGTGTAG	CCAGTCTACC	ACCACCACAG	CACCCACAGC	AGCTAGGCTT	AGCCCCTCTG	840
CTTCCCTTC	ATTGTACT					858

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: 969170

Met 1	Gly	Lys	Tyr	Cys 5	Ala	Ser	Leu	Gly	Val 10	Leu	Lys	Gly	Pro	Trp 15	Asp
Gln	Val	Phe	Ala	Ala	Phe	Trp	Gln	Arg	Tyr	Pro	Asn	Pro	Tyr	Ser	Lys
			20					25					30		
His	Val	Leu	Thr	Glu	Asp	Ile	Val	His	Arg	Glu	Val	Thr	Ala	Asp	His
		35					40					45			
Lys	Leu	Leu	Ser	Arg	Arg	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Met	Pro	Arg
	50					55					60				
Trp	Ala	Glu	Arg	Phe	Phe	Pro	Ala	Asn	Val	Ala	His	Asn	Val	Tyr	Ile
65				70					75					80	
Val	Glu	Asp	Ser	Ile	Val	Asp	Pro	Lys	Asn	Arg	Thr	Met	Thr	Thr	Phe
				85				90						95	
Thr	Trp	Asn	Ile	Asn	His	Ala	Arg	Leu	Met	Ala	Val	Glu	Glu	Arg	Cys
			100					105					110		
Val	Tyr	Arg	Val	Asn	Pro	Glu	Asn	Ser	Ser	Trp	Thr	Glu	Val	Lys	Arg
		115					120					125			
Glu	Ala	Trp	Val	Ser	Ser	Ser	Leu	Phe	Gly	Val	Ser	Arg	Ala	Val	Gln
		130				135					140				
Glu	Phe	Gly	Leu	Arg	Phe	Lys	Ser	Asn	Val	Thr	Lys	Ser	Thr	Lys	
145				150					155					160	
Gly	Phe	Glu	Tyr	Val	Leu	Ala	Arg	Met	Gln	Gly	Glu	Ala	Pro	Ser	Lys
				165					170					175	
Thr	Leu	Val	Glu	Thr	Ala	Lys	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Glu	Thr
			180					185					190		
Ala	Leu	Ala	Ala	Thr	Glu	Lys	Ala	Lys	Asp	Leu	Ala	Ser	Lys	Ala	Ala
		195					200					205			
Thr	Lys	Lys	Lys	Gln	Phe	Val									
	210					215									